

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/734,692

Source: _____

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RAW SEQUENCE LISTING DATE: 06/06/2005
PATENT APPLICATION: US/10/734,692 TIME: 08:02:11

Input Set : N:\Crf4\Reffold\10_folder\J734692.raw
Output Set: N:\CRF4\06062005\J734692.raw

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1 <110> APPLICANT: Stashenko, Philip
2 Okamatsu, Yoshimura
3 Sasaki, Hajime
4 Battaglino, Richard
5 Spaete, Ulrike
6 <120> TITLE OF INVENTION: Expressed Genes that Define the Osteoclast Phenotype
7 <130> FILE REFERENCE: 25669-003
8 <140> CURRENT APPLICATION NUMBER: US/10/734,692
9 <141> CURRENT FILING DATE: 2003-12-11
10 <150> PRIOR APPLICATION NUMBER: 60/432,700
11 <151> PRIOR FILING DATE: 2002-12-11
12 <160> NUMBER OF SEQ ID NOS: 49
13 <170> SOFTWARE: PatentIn version 3.2
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 22
17 <212> TYPE: DNA
18 <213> ORGANISM: Mus musculus
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36 agtccagagc agtctgaagg cacagcaagg gcttgaatt gaaatgttc acatgggctt 180
37 tcaagactct tcagattgt gcctgtccct taactcacgg attcagtgtt caagatttat 240
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39 ggggttccag gtctgtgccca accccagtga tcggagagtt cagagatgca ttgaaagatt 360
40 ggagaaaaac tcacaaccac ggacctacaa acaataacat ttgcctttaga gaagggtgtg 420
41 aactgccagc tactttctt ggtcttcccc agtgaccacc taagtggctc taagtgttta 480
42 ttttatagg tatataaaca ttttttttt ctgtttccac tttaaagtgg catatctggc 540
43 tttgtcacag aggggaaact tgtctgtgcc aaccccagtgc atctgaaaac tcagatgcct 600
44 gggaaaggctc gaagctgacc tcaatgacta cacataatat ttgattgaga taaatggca 660
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49	cggtttccca	gcccgtttta	agtggataaa	ctgtgagagt	ggctgtggg	actttggaa	960
50	gtgtctgggtt	ctgatagtc	cttatggcaa	cccaggatca	ttcaactagg	atgaaataaa	1020
51	ttctgcctta	gcccgttagt	atgtctgtgt	ttgttaaggac	ccagctgatt	ttccaccac	1080
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62	20 25 30						
63	Gln Ser Ser Leu Lys Ala Gln Gln Gly Leu Glu Ile Glu Met Phe His						
64	35 40 45						
65	Met Gly Phe Gln Asp Ser Ser Asp Cys Cys Leu Ser Tyr Asn Ser Arg						
66	50 55 60						
67	Ile Gln Cys Ser Arg Phe Ile Gly Tyr Phe Pro Thr Ser Gly Gly Cys						
68	65 70 75 80						
69	Thr Arg Pro Gly Ile Ile Phe Ile Ser Lys Arg Gly Phe Gln Val Cys						
70	85 90 95						
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84	tgtactcctt ggtatttgc attggcctgg ttggAACAT cctgggtggtc ctggccttg						240
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91	accacacctg cagccttcac tttcctcagc aaagcctacg agagtggaa ctgtttcagg						660
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93	caggattat aaagattctg ctaagacgac caaatgagaa gaaatccaa gctgtccgtt						780
94	tgatTTTGT catcatgatc atcttttttcc tctttggac cccctacaat ttgactatac						840
95	ttatTTCTGT tttccaagac ttctgttca cccatgagtg tgagcagagg agacattgg						900
96	acctggctgt gcaagtgcg gaggtgtatcg cctacacgca ctgtgtgtc aacccagtga						960
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100	aggaggccaa	ccccaaataaa	gcaggcgtga	cctgccaggc	acactgagcc	agcagcctgg	1200									
101	ctctcccagc	caggttctga	ctcttggcac	agcatggagt	cacagccact	tggatagag	1260									
102	aggaaatgta	atggtggcct	ggggcttctg	aggcttctgg	ggcttcagtc	ttttccatga	1320									
103	acttctcccc	tggtagaaag	aagatgaatg	agcaaaacca	aatattccag	agactgggac	1380									
104	taagtgtacc	agagaaggc	ttggactcaa	gcaagatttc	agatttgtga	ccattagcat	1440									
105	ttgtcaacaa	agtcacccac	ttcccactat	tgcttgcaca	aaccaattaa	acccagtagt	1500									
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107	gaatttctgt	tcttccatca	cctccccccc	cccgccaccc	tcccactgcc	aagaacttgg	1620									
108	aaatagtat	ttccacagtg	actccactct	gagtcccaga	gccaatcaat	agccagcatc	1680									
109	tgcctccccc	tcactccac	cgcaggattt	gggcttctgg	aatcctgggg	aacatagaac	1740									
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111	ggaactaaga	aagcccttag	gaagaatttt	tatattccact	aaaatcaaac	aattcaggga	1860									
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113	gagggactca	tcattttccat	ttacccttct	tttctgacta	tttttcagaa	tctcttct	1980									
114	tttcaagttg	ggtgatatgt	tggtagattc	taatggctt	attgcagcga	ttaataaacag	2040									
115	gcaaaaaggaa	gcagggttgg	tttcccttct	ttttgttctt	catctaagcc	ttctggttt	2100									
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128						35			40					45		
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130						50			55					60		
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132						65			70					75		80
133	Leu	Leu	Phe	Leu	Phe	Thr	Leu	Pro	Phe	Trp	Ile	Asp	Tyr	Lys	Leu	Lys
134						85			90					95		
135	Asp	Asp	Trp	Val	Phe	Gly	Asp	Ala	Met	Cys	Lys	Ile	Leu	Ser	Gly	Phe
136						100			105					110		
137	Tyr	Tyr	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr
138						115			120					125		
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140						130			135					140		
141	Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Ile	Ile	Trp	Ala	Leu
142						145			150					155		160
143	Ala	Ile	Leu	Ala	Ser	Met	Pro	Gly	Leu	Tyr	Phe	Ser	Lys	Thr	Gln	Trp
144						165			170					175		
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152	225	230	235
153	Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn		
154	245	250	255
155	Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu		
156	260	265	270
157	Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val		
158	275	280	285
159	Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val		
160	290	295	300
161	Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val		
162	305	310	315
163	Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu		
164	325	330	335
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185	accacacctg cagccttcac tttcctcactg aaagcctacg agagtgaaag ctgttccagg	660	
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187	cagggattat aaagattctg ctaagacgac caaatgagaa gaaatccaa gctgtccgtt	780	
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194	aggaggccaa cccaaaataa gcaggcgta cctgccaggc acactgagcc agcagcctgg	1200	
195	ctctcccacg caggttctga ctcttggcac agcatggagt cacagccact tggatagag	1260	
196	aggaaatgt aatggtggctt gggcttctgt aggcttctgg ggcttcagtc tttccatga	1320	
197	acttctcccc tggtagaaag aagatgaatg agcaaaaccca aatattccag agactggac	1380	

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200	ggtgactgtg	ggctccattc	aaagtggact	cctaagccat	gggagacact	gatgtatgag	1560									
201	gaatttctgt	tttccatca	cctcccccc	cccgcaccc	tcccactgcc	aagaacttgg	1620									
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203	tgcctccct	tcactcccac	cgcaggattt	gggcttgg	aatcctggg	aacatagaac	1740									
204	tcatgacgga	agagttgaga	cctaacgaga	aatagaaatg	ggggactac	tgctggcagt	1800									
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209	gaaaaaggaa	gcagggttgg	ttcccttct	ttttttctt	catctaagcc	ttctggttt	2100									
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222						35			40			45				
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224						50			55			60				
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227	Leu	Leu	Phe	Leu	Phe	Thr	Leu	Pro	Phe	Trp	Ile	Asp	Tyr	Lys	Leu	Lys
228						85			90			95				
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230						100			105			110				
231	Tyr	Tyr	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr
232						115			120			125				
233	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala
234						130			135			140				
235	Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Ile	Ile	Trp	Ala	Leu
236						145			150			155			160	
237	Ala	Ile	Leu	Ala	Ser	Met	Pro	Gly	Leu	Tyr	Phe	Ser	Lys	Thr	Gln	Trp
238						165			170			175				
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240						180			185			190				
241	Arg	Glu	Trp	Lys	Leu	Phe	Gln	Ala	Leu	Lys	Leu	Asn	Leu	Phe	Gly	Leu
242						195			200			205				
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246						225			230			235			240	
247	Ile	Phe	Val	Ile	Met	Ile	Ile	Phe	Phe	Phe	Trp	Thr	Pro	Tyr	Asn	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:48; N Pos. 5,6,7

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:28,29

VERIFICATION SUMMARY

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Input Set : N:\Crf4\Reffold\10_folder\J734692.raw
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L:327 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0